Identification of Novel Regions of Allelic Loss From a Genomewide Scan of Esophageal Squamous-Cell Carcinoma in a High-Risk Chinese Population

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Abstract: Esophageal cancer is one of the most common fatal cancers worldwide. Deletions of genomic regions are thought to be important in esophageal carcinogenesis. We conducted a genomewide scan for regions of allelic loss using microdissected DNA from II esophageal squamous-cell carcinoma patients with a family history of upper gastrointestinal tract cancer from a high-risk region in north central China. Allelic patterns of 366 fluorescently labeled microsatellite markers distributed at 10-cM intervals over the 22 autosomal chromosomes were examined. We identified 14 regions with very high frequency ($\geq$ 75%) loss of heterozygosity (LOH) including broad regions encompassing whole chromosome arms (on 3p 5q 9p, 9q, and 13q), regions of intermediate size (on 2q, 4p, 11p, and 15q), and more discrete regions identified by very high frequency LOH for a single marker (on 4q, 6q, 6p. 14q. and 17p). Among these 14 regions were 7 not previously described in esophageal squamous-cell carcinoma as having very high frequency LOH (on 2q, 4p. 4q, 6q, 8p, 14q, and 15q). The very high frequency LOH regions identified here may point to major susceptibility genes. including potential tumor suppressor genes and inherited gene loci, which will assist in understanding the molecular events involved in esophageal carcinogenesis and may help in the development of markers for genetic susceptibility testing and screening for the early detection of this cancer.